

Figure 1

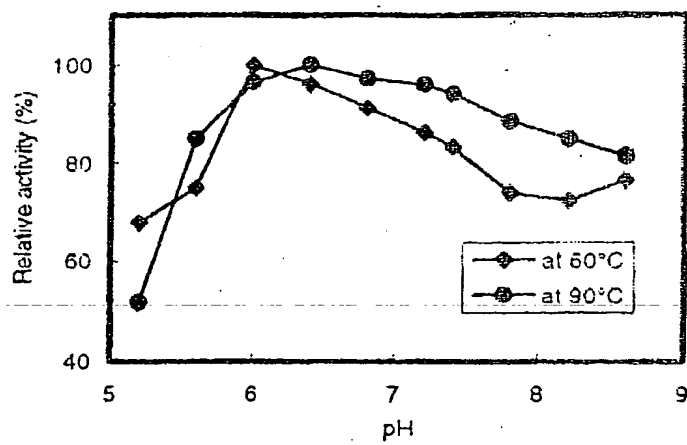
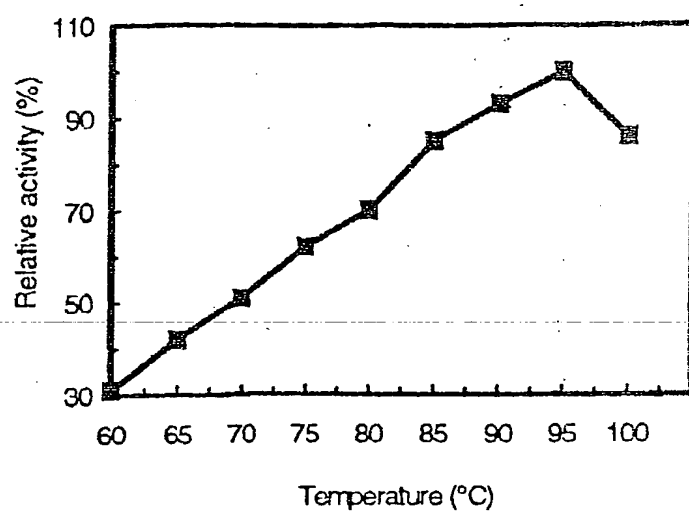
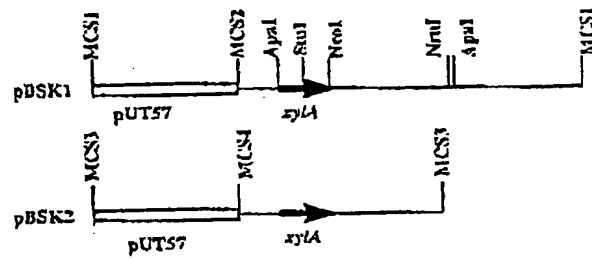
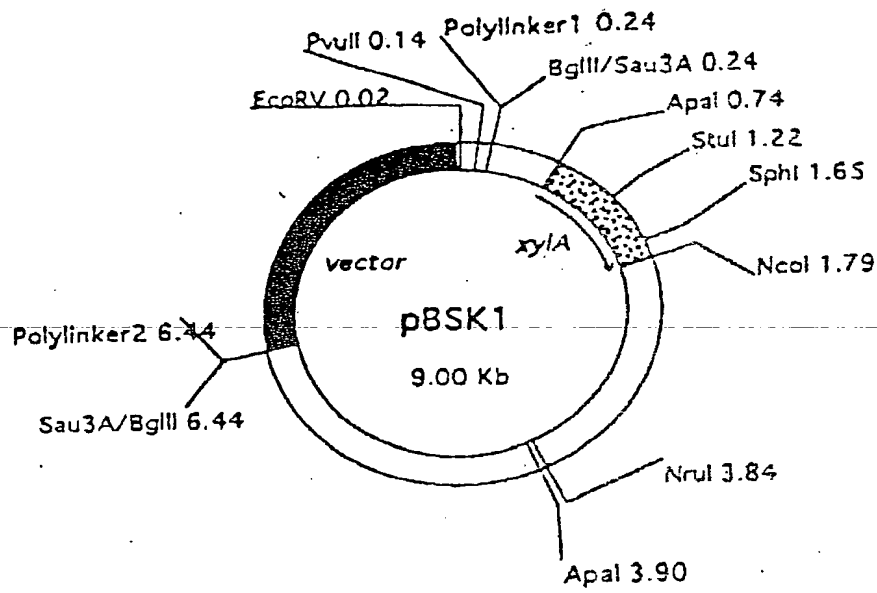


Figure 2



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Figure 3



CACGAGCGCC TTGGTGAGCTGGGTGGACGAGTCCACACGAGACGAGCGGACCGTGGCTGGATCGACATCGGCTCCTCCCTTCCTCCGGCTCAGGGG	100
CTCTGACCTGGCGCTTCACGCTATGCGGGGCC TG TGGGCCCCGGGTGCGGACCGCGCCGGCGGCTTCTGCTTCGCGCTTCCCTTCCAGGGACGCGGC	200
TVGGCATACTAATTGTAAATCGCCCTGAGCGAAATAGTCGCAAGCGAGCAAGGAGCGCGGATGCACTACCAGGCCACCCCGAGGACAGGTTACCTT	300
M N Y Q P T P E D R F T F	13
CGCCCTGTGGACCGTTCGCTGGCGAGCGGCGGGAACCCCTTGGGCGACCGGCAGCGCTCGCCCTTGAGCGCGGTGATGTCGACGCGGCTGGCGGAACGGGC	400
G L W T V G W Q C R D P F G D A T R P A L D P V D V Q R L A E L G	46
GGCTACGGAGTGACCTTCCACGAGCAGCAGCTGATTCCTCTTGGGGCGTTCGACACCGAGCGCGAGGCGCACGCTCAAGCGGTTCCGCTCAGGCGCTCGACG	500
A Y G V T F H D D D L I P F G A S D T E R E A H V K R F R Q A L D	79
CGACCGGCATGACCGTTCGATGGCGACCAACCACTCTTTCACCCACCCCGCTTTCAGGCGAGGCGGTTTCACGCGCAACGACCCCGCAGTGGCGCGCTTA	600
A T G H T V P M A T T N L F T H P V F K A G A F T A N D R A V R R Y	113
CGCCCTGGCCAAAGACCATTCGGAACATGATCTCGCGGTGAGGCTGGGCGCAAGGCTACGCTCGCTCGGGCGGCGCGAGGCGCGGAGTCCGGTGCC	700
A L R K T I R N I D L A V E L G A K V Y V A W G G R E G A E S G A	146
GCCAAGGACGTGCGTGGCGCCCTGGACCGCATGAAGGAGGCTTCGACCTGCTCGCGGAGTACGTCACCTCGCAGGCGTACGACATCCGGTTCCGCATCG	800
A K D V R A A L D R M K E A F D L L G E Y V T S Q G Y D I R F A I	179
AGCCCAAGCGGAACGAGCGCGCGCGGACATCTGCTGCGCACCATCGGCCACCGCGCTCGCGTTTCATGAGCGCGCTCGAGCGCGCGGAGCTGTACGGTGT	900
E P K P N E P R G D I L L P T I G H A L A F I E R L E R K P E L Y G V	213
CAACCCCGAGGTGGGGCACGAGCAGATGGCGGCTGAAGTTCGCGCACGGCATCGCGAGGCTCTGTGGGCGGCGAAGCTCTTCACATGAGCTCAAC	1000
N P E V G H E Q M A G L N F P H G I A Q A L W A G K L F H I D L N	246
GGCCAGTCCGGCATCAAGTACGACCAAGGACCTGGCGCTTCGGCGCGCGGTGACCTGGCGCGCGGCTTCTGCTGGTTCGACCTGCTTCGAGAGCGCGCGCTGGG	1100
G Q S G I K Y D Q D L R F G A G D L R A A P H L V D L L E S A G W	289
AGGGTCCGCGCCACTTCGACTCAAGSCCCCGCGGACCGAGGACATCGACCGCGTGTGGGCTTCGCGCGCGGSGTGCATGCGCAACTACCTGATCTTGAA	1200
E G P R H F D P K P P R T E D I D G V W A S A A G C M R N Y L I L K	313
CGAGCGCGCGCGCGCTTCGCTGGCGACCGCGGAGGTCCAGGAGGCGCTCGCTGCGCGCGCGCTGACCAAGCTCGCGGAGCCACCGCGGCGCAGCGGCTG	1300
E R A A A A F R A D P E V Q E A L R A R L D Q L A E P T A A D G L	346
CAGGCGCTGCTGGCGCGACCGCACCGGCTACGAGGACTTCGACGTGGACGCGCGCGCGCGCGGATGCGCTTCGAGCGGCTCGACCACTCGCCATGGACC	1400
Q A L L A D R T A Y E D F D V D A A A R G M A F E R L D Q L A M D	379
ACCTGCTGGGCGCGCGCGCTCAACCGGGGACGAGGGGGTACGCGCGGTTCGATCTCCCTCGCTGCTCATGAGGGGGTGTGCGCGCGCTCGAGGCGCGCC	1500
H L L G A R G ***	386
GGCCCCATCGTGTCTCGCTCTCCCGCGCGCGGTGTGGGCGCGCTGC	1546

[illegible]

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112

C	XYLA-STRSK	99-A <sub>100</sub> -G-A <sub>102</sub> -FTANDR-A <sub>109</sub> -VRR- <del>113</del>	112
C	XYLA-STROL	99-D <sub>100</sub> -G-G <sub>102</sub> -FTANDR-D <sub>109</sub> -VRR- <del>113</del>	112
C	XYLA-STRVO	99-D <sub>100</sub> -G-G <sub>102</sub> -FTANDR-D <sub>109</sub> -VRR- <del>113</del>	112
C	XYLA-ACTMI	99-D <sub>100</sub> -G-G <sub>102</sub> -FTSNDR-S <sub>109</sub> -VRR- <del>113</del>	112
C	XYLA-AMPSP	99-D <sub>100</sub> -G-G <sub>102</sub> -FTSNDR-S <sub>109</sub> -VRR- <del>113</del>	112
C	XYLA-THETH	99-D <sub>100</sub> -G-A <sub>102</sub> -FTSPDP-W <sub>109</sub> -VRA- <del>111</del>	112

[illegible]